

HUMAN CYTOSKELETON ASSOCIATED PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human cytoskeleton associated proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders.

BACKGROUND OF THE INVENTION

The cytoskeleton, a cytoplasmic system of protein fibers, mediates cell shape, structure, and movement. The cytoskeleton supports the cell membrane and forms tracks along which organelles and other elements move in the cytosol. The cytoskeleton is a dynamic structure that allows cells to adopt various shapes and to carry out directed movements. Major cytoskeletal fibers are the microfilaments, the microtubules, and the intermediate filaments. Motor proteins, including myosin, dynein, and kinesin, drive movement of, or along, the fibers. The motor protein dynamin drives the formation of membrane vesicles. Accessory or associated proteins modify the structure or activity of the fibers while cytoskeletal membrane anchors connect the fibers to the cell membrane. (The cytoskeleton is reviewed in Lodish, H. et al. (1995) Molecular Cell Biology Scientific American Books, New York NY.)

Microtubules and Associated Proteins

Tubulins

Microtubules, cytoskeletal fibers with a diameter of 24 nm, have multiple roles in the cell. Bundles of microtubules form cilia and flagella, which are whip-like extensions of the cell membrane that are necessary for sweeping materials across an epithelium and for swimming of sperm, respectively. Marginal bands of microtubules in red blood cells and platelets are important for these cells' pliability. Organelles, membrane vesicles, and proteins are transported in the cell along tracks of microtubules. For example, microtubules run through nerve cell axons, allowing bi-directional transport of materials and membrane vesicles between the cell body and the nerve terminal. Failure to supply the nerve terminal with these vesicles blocks the transmission of neural signals. Microtubules, in the form of the spindle, are also critical to chromosomal movement during cell division. Both stable and short-lived populations of microtubules exist in the cell.

Microtubules are a polymer of GTP-binding tubulin protein subunits. Each subunit is a heterodimer of α - and β - tubulin, multiple isoforms of which exist. The hydrolysis of GTP is linked

to the addition of tubulin subunits at the end of a microtubule. The subunits interact head to tail to form protofilaments; the protofilaments interact side to side to form a microtubule. A microtubule is polarized, one end ringed with α -tubulin and the other with β -tubulin, and the two ends differ in their rates of assembly. Generally each microtubule is composed of 13 protofilaments although 11 or 15 protofilament-microtubules are sometimes found. Cilia and flagella contain doublet microtubules. Microtubules grow from specialized structures known as centrosomes or microtubule-organizing centers (MTOCs). MTOCs may contain one or two centrioles, which are pinwheel arrays of triplet microtubules. The basal body, the organizing center located at the base of a cilium or flagellum, contains one centriole. γ -tubulin present in the MTOC is important for nucleating the polymerization of α - and β -tubulin heterodimers but does not polymerize into microtubules. The protein pericentrin is found in the MTOC and has a role in microtubule assembly.

Microtubule-Associated Proteins

Microtubule-associated proteins (MAPs) have roles in the assembly and stabilization of microtubules. One major family of MAPs, assembly MAPs, can be identified in neurons as well as non-neuronal cells. Assembly MAPs are responsible for cross-linking microtubules in the cytosol. These MAPs are organized into two domains: a basic microtubule-binding domain and an acidic projection domain. The projection domain is the binding site for membranes, intermediate filaments, or other microtubules. Based on sequence analysis, assembly MAPs can be further grouped into two types: Type I and Type II.

Type I MAPs, which include MAP1A and MAP1B, are large, filamentous molecules that copurify with microtubules and are abundantly expressed in brain and testis. They contain several repeats of a positively-charged amino acid sequence motif that binds and neutralizes negatively charged tubulin, leading to stabilization of microtubules. MAP1A and MAP1B are each derived from a single precursor polypeptide that is subsequently proteolytically processed to generate one heavy chain and one light chain.

Another light chain, LC3, is a 16.4 kDa molecule that binds MAP1A, MAP1B, and microtubules. It is suggested that LC3 is synthesized from a source other than the MAP1A or MAP1B transcripts, and the expression of LC3 may be important in regulating the microtubule binding activity of MAP1A and MAP1B during cell proliferation (Mann, S. S. et al. (1994) J. Biol. Chem. 269:11492-11497).

Type II MAPs, which include MAP2a, MAP2b, MAP2c, MAP4, and Tau, are characterized by three to four copies of an 18-residue sequence in the microtubule-binding domain. MAP2a, MAP2b, and MAP2c are found only in dendrites, MAP4 is found in non-neuronal cells, and Tau is found in axons and dendrites of nerve cells. Alternative splicing of the Tau mRNA leads to the

existence of multiple forms of Tau protein. Tau phosphorylation is altered in neurodegenerative disorders such as Alzheimer's disease, Pick's disease, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia and Parkinsonism linked to chromosome 17. The altered Tau phosphorylation leads to a collapse of the microtubule network and the formation of
5 intraneuronal Tau aggregates (Spillantini, M.G. and Goedert, M. (1998) Trends Neurosci. 21:428-433).

Tektins are filamentous proteins that were originally discovered in association with axonemal microtubules of sea urchin sperm. Subsequent work has shown that tektins are also found in association with spindle microtubules in clams and in mammals. (Steffen, W. and Linck, R.W.
10 (1992) J. Cell Sci. 101:809-822.) Tektins may form rod-like alpha-helical structures similar to those of intermediate filament proteins (Norrandner, J.M. et al. (1996) J. Mol. Biol. 29:385-397).

Microtubular aggregates are associated with several disorders. An extraskeletal myxoid chondrosarcoma tumor from human contained parallel arrays of microtubules within the rough endoplasmic reticulum (Suzuki, T. et al. (1988) J. Pathol. 156:51-57). Microtubular aggregates were
15 also found in hepatocytes from chimpanzees infected with hepatitis C virus. Monoclonal antibodies prepared to these aggregates detect a protein called p44 (or microtubular aggregates protein) (Maeda, T. et al. (1989) J. Gen. Virol. 70:1401-1407). A human homolog of p44 is inducible by interferon- α and interferon- β , but not by interferon- γ . p44 protein may be a mediator in the antiviral action of interferon (Kitamura, A. et al. (1994) Eur. J. Biochem. 224:877-883).

20 Dynein-related Motor Proteins

Dyneins are (-) end-directed motor proteins which act on microtubules. Two classes of dyneins exist, cytosolic and axonemal. Cytosolic dyneins are responsible for translocation of materials along cytoplasmic microtubules, for example, transport from the nerve terminal to the cell body and transport of endocytic vesicles to lysosomes. Cytoplasmic dyneins are also reported to play
25 a role in mitosis. Axonemal dyneins are responsible for the beating of flagella and cilia. Dynein on one microtubule doublet walks along the adjacent microtubule doublet. This sliding force produces bending forces that cause the flagellum or cilium to beat. Dyneins have a native mass between 1000 and 2000 kDa and contain either two or three force-producing heads driven by the hydrolysis of ATP. The heads are linked via stalks to a basal domain which is composed of a highly variable number of
30 accessory intermediate and light chains.

Microfilaments and Associated Proteins

Actins

Microfilaments, cytoskeletal filaments with a diameter of 7-9 nm, are vital to cell locomotion.

cell shape, cell adhesion, cell division, and muscle contraction. Assembly and disassembly of the microfilaments allow cells to change their morphology. Microfilaments are the polymerized form of actin, the most abundant intracellular protein in the eukaryotic cell. Human cells contain six isoforms of actin. The three α -actins are found in different kinds of muscle, nonmuscle β -actin and nonmuscle γ -actin are found in nonmuscle cells, and another γ -actin is found in intestinal smooth muscle cells. G-actin, the monomeric form of actin, polymerizes into polarized, helical F-actin filaments, accompanied by the hydrolysis of ATP to ADP. Actin filaments associate to form bundles and networks, providing a framework to support the plasma membrane and determine cell shape. These bundles and networks are connected to the cell membrane. In muscle cells, thin filaments containing actin slide past thick filaments containing the motor protein myosin during contraction. A family of actin-related proteins exist that are not part of the actin cytoskeleton, but rather associate with microtubules and dynein.

Actin-Associated Proteins

Actin-associated proteins have roles in cross-linking, severing, and stabilization of actin filaments and in sequestering actin monomers. Several of the actin-associated proteins have multiple functions. Bundles and networks of actin filaments are held together by actin cross-linking proteins. These proteins have two actin-binding sites, one for each filament. Short cross-linking proteins promote bundle formation while longer, more flexible cross-linking proteins promote network formation. Calmodulin-like calcium-binding domains in actin cross-linking proteins allow calcium regulation of cross-linking. Group I cross-linking proteins have unique actin-binding domains and include the 30 Kd protein, EF-1a, fascin, and scruin. Group II cross-linking proteins have a 7,000-MW actin-binding domain and include villin and dematin. Group III cross-linking proteins have pairs of a 26,000-MW actin-binding domain and include fimbrin, spectrin, dystrophin, ABP 120, and filamin.

Severing proteins regulate the length of actin filaments by breaking them into short pieces or by blocking their ends. Severing proteins include gCAP39, severin (fragmin), gelsolin, and villin. Capping proteins can cap the ends of actin filaments, but cannot break filaments. Capping proteins include CapZ, tropomodulin, and tensin.

Tensin, which is found in focal adhesions, also crosslinks actin filaments. Integrin activation by the extracellular matrix leads to the phosphorylation of tensin on tyrosine, serine, and threonine residues; this phosphorylation also occurs in cells transformed with oncogenes. Tensin has an SH2 domain and may bind to other tyrosine-phosphorylated proteins. (Lo, S.H. et al. (1997) J. Cell Biol. 136:1349-1361.) The N-terminus of tensin contains a region homologous to the catalytic domain of a putative tyrosine phosphatase (PTP) from Saccharomyces cerevisiae. This PTP domain in tensin may

mediate binding interactions with phosphorylated polypeptides (Haynie, D.T. and Ponting, C.P. (1996) Protein Sci. 5:2643-2646). Mice which lack the tensin gene have kidney abnormalities, indicating that the loss of tensin leads to weakening of focal adhesions in the kidney (Lo, supra).

The proteins thymosin and profilin sequester actin monomers in the cytosol, allowing a pool
5 of unpolymerized actin to exist. Profilin may also stimulate F-actin formation by effectively lowering the critical concentration required for actin monomer addition (Gertler, F.B. et al. (1996) Cell 87:227-239).

The Ena/VASP (vasodilator-stimulated phosphoprotein) protein family has roles in actin-based motility. These proteins, including Mena, VASP, and Evl (Ena/VASP-like), have homology to
10 the Drosophila Enabled protein which is involved in neural development. Mammalian Ena/VASP proteins localize at focal contacts and in regions where actin filaments are highly dynamic. The neural forms of Mena induce F-actin rich outgrowths in fibroblasts. Mena may have roles in microfilament-based extension of filopodia during axonal growth cone migration. In vitro motility assays of the intracellular pathogenic bacterium Listeria monocytogenes in platelet and brain extracts
15 show that the Ena/VASP proteins play interchangeable roles in the transformation of actin polymerization into active movement and propulsive force. The Ena/VASP proteins associate with actin, profilin, the focal adhesion protein zyxin, and vinculin. Phosphorylation of Mena and VASP may regulate their activity. (Gertler, supra; Laurent, V. et al. (1999) J. Cell Biol. 144:1245-1258.)

The actin-associated proteins tropomyosin, troponin, and caldesmon regulate muscle
20 contraction in response to calcium. The tropomyosin proteins, found in muscle and nonmuscle cells, are α -helical and form coiled-coil dimers. Striated muscle tropomyosin mediates the interactions between the troponin complex and actin, regulating muscle contraction. (PROSITE PDOC00290 Tropomyosins signature.) The troponin complex is composed of troponin-T, troponin-I, and troponin-C. Troponin-T binds tropomyosin, linking troponin-I and troponin-C to tropomyosin.

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Intermediate Filaments and Associated Proteins

Intermediate filaments (IFs) are cytoskeletal fibers with a diameter of 10 nm, intermediate between that of microfilaments and microtubules. They serve structural roles in the cell, reinforcing cells and organizing cells into tissues. IFs are particularly abundant in epidermal cells and in neurons.
30 IFs are extremely stable, and, in contrast to microfilaments and microtubules, do not function in cell motility. IF proteins include acidic keratins, basic keratins, desmin, glial fibrillary acidic protein, vimentin, peripherin, neurofilaments, nestin, and lamins.

IFs have a central α -helical rod region interrupted by short nonhelical linker segments. The rod region is bracketed, in most cases, by non-helical head and tail domains. The rod regions of

intermediate filament proteins associate to form a coiled-coil dimer. A highly ordered assembly process leads from the dimers to the IFs. Neither ATP nor GTP is needed for IF assembly, unlike that of microfilaments and microtubules.

IF-associated proteins (IFAPs) mediate the interactions of IFs with one another and with other cell structures. IFAPs cross-link IFs into a bundle, into a network, or to the plasma membrane, and may cross-link IFs to the microfilament and microtubule cytoskeleton. Microtubules and IFs in particular are closely associated. IFAPs include BPAG1, plakoglobin, desmoplakin I, desmoplakin II, plectin, ankyrin, filaggrin, and lamin B receptor.

The N-terminal portion of ankyrin consists of a repeated 33-amino acid motif, the ankyrin repeat, which is involved in specific protein-protein interactions. Variable regions within the motif are responsible for specific protein binding, such that different ankyrin repeats are involved in binding to tubulin, anion exchange protein, voltage-gated sodium channel, Na^+/K^+ -ATPase, and neurofascin. The ankyrin motif is also found in transcription factors, such as NF- κ -B, and in the yeast cell cycle proteins CDC10, SW14, and SW16. Proteins involved in tissue differentiation, such as *Drosophila* Notch and *C. elegans* LIN-12 and GLP-1, also contain ankyrin-like repeats. Lux et al. (1990; Nature 344:36-42) suggest that ankyrin-like repeats function as 'built-in' ankyrins and form binding sites for integral membrane proteins, tubulin, and other proteins.

Other Cytoskeleton-Associated Proteins

Some cytoskeleton-associated proteins contain a conserved, glycine-rich domain of about 42 residues. This domain, called CAP-Gly, is found in restin, a protein associated with intermediate filaments; vertebrate dynactin, which is associated with dynein; and yeast BIK1 protein which may be required for the formation or stabilization of microtubules during mitosis and for spindle pole body fusion during conjugation. (PROSITE PDOC00660 CAP-Gly domain signature.)

Proteins of the Erythrocyte Membrane Skeleton

Distribution of oxygen throughout the vertebrate body is effected by red blood cells (erythrocytes). Oxygen diffuses from surrounding water or from the atmosphere through either gill epithelium or pulmonary epithelial type I cells. Oxygen then diffuses through the blood capillary endothelium directly to the blood circulatory system and through the erythrocyte membrane and is stored as soluble oxyhemoglobin in the cytoplasm. Oxygen is released from hemoglobin at sites throughout the organism and diffuses out from the erythrocyte to other target cells. The structure of the erythrocyte membrane as well as that of other non-erythrocyte cells must be maintained to enable efficient diffusion of oxygen to intracellular compartments.

The erythrocyte membrane is comprised of i) a cholesterol-rich phospholipid bilayer in which many trans-bilayer proteins are embedded, ii) external glycosylphosphatidylinositol-anchored proteins (GPI-proteins), and iii) the erythrocyte or membrane skeleton that laminates the inner surface of the bilayer. The trans-bilayer proteins include anion exchangers, glycophorins, glucose transporters, and a variety of cation transporters and pumps. The erythrocyte GPI-proteins include acetylcholinesterase and decay-accelerating factor (CD 55). The skeletal proteins are organized on the cortical, or cytoplasmic, face of the plasma membrane. These proteins include protein 4.1, protein p55, α - and β -spectrin, actin, and actin-binding proteins such as dematin, tropomyosin, and tropomodulin. α - and β -spectrin combine to form a heterotetramer *in vivo*. The spectrin heterotetramer organizes into a cortical bidimensional network with a hexagonal mesh. The network is linked to trans-bilayer proteins through a protein complex comprising β -spectrin, ankyrin, anion exchanger, and protein 4.2 and through the "triangular" interaction between protein 4.1, glycophorin C, and protein p55. Structural and functional variants of erythrocyte membrane proteins have been found in a variety of tissues. Variants may be transcribed from multigene families, e.g., anion exchanger, ankyrin, or spectrin, or from single gene families, e.g., protein 4.1 or protein 4.2. mRNA transcripts undergo tissue-specific alternative splicing. Many congenital hemolytic anemias result from mutations in the above-mentioned genes encoding erythrocyte membrane proteins. For example, hereditary elliptocytosis stems from an array of mutations in the spectrin genes at or near the head-to-head self-association region of the spectrin tetramer, or from mutations in the protein 4.1 gene which reduce levels of protein 4.1. In another example, hereditary spherocytosis is associated with mutations in the ankyrin gene, the anion exchanger gene, the protein 4.2 gene, or the α - and β -spectrin genes. (Delaunay J. (1995) Transfus. Clin. Biol. 2:207-216.)

Protein 4.1 is an 80 kDa erythrocyte membrane protein with four functional domains. These domains include: i) a 30 kDa basic N-terminal domain, homologous to the ERM (Ezrin/Radixin/Moesin) family of actin- and transmembrane protein-binding proteins (Tsukita, S. et al. (1997) Trends Biochem. Sci. 22:53-58); ii) a 16 kDa hydrophilic domain containing a protein kinase C phosphorylation site; iii) a 10 kDa highly charged domain containing a cAMP-dependent protein kinase phosphorylation site critical for the interaction with spectrin and actin; and iv) a 22/24 kDa acidic domain. Protein 4.1 is a member of a structurally and functionally related protein 4.1 family. The protein 4.1 family is part of an evolutionarily related protein superfamily that includes many tyrosine phosphatases. (Baklouti, F. et al. (1997) Genomics 39:289-302.)

In contrast to the strictly cortical localization of protein 4.1 in mature enucleate erythrocytes, protein 4.1 epitopes have been observed throughout the cytoplasmic compartment and the nucleoskeleton in nucleated cells. In particular, protein 4.1 is present in the nucleoskeleton during

interphase, in the mitotic spindle during mitosis, in perichromatin during telophase, and in the midbody during cytokinesis. (Krauss, S.W. et al. (1997) J. Cell Biol. 137:275-289.)

Differential expression of the protein 4.1 gene resulting in a number of mRNA splice variants has been observed in various human and rodent tissues. Comparison of the gene structure and mRNA
5 splice variants revealed the extreme genomic sequence conservation of protein 4.1 between different species. The 5' UTR of both the human and rodent mRNA species has not been successfully identified and sequenced, possibly due to GC-rich regions therein which give rise to technical complications during nucleotide sequencing reactions. (Baklouti, supra; Conboy, J.G. (1988) Proc. Natl. Acad. Sci. 85:9062-9065.)

10 Analysis of proteins included in the ERM family of proteins has indicated that the N-terminal domain interacts with intracellular domains of transmembrane proteins such as CD44 and the C-terminal domain binds actin. Both interactions involve interactions with Rho-GTP protein complex, polyphosphoinositides, and serine/threonine kinase and tyrosine kinase activities. Many of the phosphorylation sites on ERM proteins are conserved. Although expression of ERM proteins in vivo
15 is restricted to tissues such as endothelium, repression of ERM protein gene expression is released under conditions of cell culture. (Tsukita, supra.)

The cortical actin cytoskeleton participates in various membrane-based processes which necessitate a large amount of functional plasticity in the molecular components involved. A family of proteins homologous to band 4.1 is involved in the reorganization of the actin cytoskeleton in
20 response to various stimuli and probably plays a role in transmembrane signaling. This family includes tyrosine phosphatases, substrates of tyrosine kinases and a candidate for a tumor-suppressor gene. (Arpin M, et al. (1994) Curr. Opin. Cell Biol. 6:136-141.)

Disruptions in cytoskeletal protein interaction have been identified in a number of disease conditions or disorders. Neurofibromatosis type 2 is an autosomal dominant disease of the nervous
25 system. Schwann cells isolated from patients with neurofibromatosis type 2 have characteristic morphology and growth parameters which differ from control Schwann cells. A gene associated with neurofibromatosis type 2 has been identified and is termed NF2. The NF2 gene product, known as schwannomin or merlin, is a member of the protein 4.1 superfamily, and mutations in the NF2 gene have been shown to be associated with the disease. (Rosenbaum, C. et al. (1998) Neurobiol. Dis.
30 5:55-64.) In addition, a form of psoriasis may be due to altered expression or distribution in epidermal epithelium of analogs of erythrocyte protein 4.1. (Shimizu, T. (1996) Histol. Histopathol. 11:495-501.) Erythrocytes carrying mutations in spectrin and protein 4.1 showed differing sensitivities to invasion by Plasmodium falciparum. (Facer, C.A. (1995) Parasitol Res. 81:52-57.) Furthermore, antibodies raised against erythrocyte protein 4.1 stained the majority of neurofibrillary

tangles in the prefrontal cortex and hippocampus of brain tissue from patients with Alzheimer's disease. A 68 kDa protein was identified as the most likely brain analog of erythrocyte protein 4.1. (Sihag, R.K. et al. (1994) Brain Res. 656:14-26.)

The discovery of new human cytoskeleton associated proteins and the polynucleotides
5 encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders.

SUMMARY OF THE INVENTION

10 The invention features substantially purified polypeptides, human cytoskeleton associated proteins, referred to collectively as "CYSKP" and individually as "CYSKP-1," "CYSKP-2," "CYSKP-3," "CYSKP-4," "CYSKP-5," "CYSKP-6," "CYSKP-7," "CYSKP-8," "CYSKP-9," "CYSKP-10," "CYSKP-11," "CYSKP-12," "CYSKP-13," "CYSKP-14," "CYSKP-15," and "CYSKP-16." In one aspect, the invention provides a substantially purified polypeptide comprising
15 an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof.

The invention further provides a substantially purified variant having at least 90% amino acid identity to at least one of the amino acid sequences selected from the group consisting of SEQ ID NO:1-16 and fragments thereof. The invention also provides an isolated and purified polynucleotide
20 encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof.

25 Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence
30 selected from the group consisting of SEQ ID NO:1-16 and fragments thereof.

The invention also provides a method for detecting a polynucleotide in a sample containing nucleic acids, the method comprising the steps of (a) hybridizing the complement of the polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the

hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:17-32, and fragments thereof. The invention further provides an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide sequence selected from the group consisting of SEQ ID NO:17-32 and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:17-32 and fragments thereof.

The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof. In another aspect, the expression vector is contained within a host cell.

The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide selected from the group consisting of SEQ ID NO:1-16 and fragments thereof. The invention also provides a purified agonist and a purified antagonist to the polypeptide.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of CYSKP, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of CYSKP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-16 and fragments thereof.

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding CYSKP.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods and algorithms used for identification of CYSKP.

Table 3 shows selected fragments of each nucleic acid sequence; the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding CYSKP were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze CYSKP, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"CYSKP" refers to the amino acid sequences of substantially purified CYSKP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or
5 recombinant.

The term "agonist" refers to a molecule which, when bound to CYSKP, increases or prolongs the duration of the effect of CYSKP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of CYSKP.

An "allelic variant" is an alternative form of the gene encoding CYSKP. Allelic variants may
10 result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one
15 or more times in a given sequence.

"Altered" nucleic acid sequences encoding CYSKP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as CYSKP or a polypeptide with at least one functional characteristic of CYSKP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide
20 probe of the polynucleotide encoding CYSKP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding CYSKP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent CYSKP. Deliberate amino acid substitutions may be made on the basis of similarity in
25 polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of CYSKP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine;
30 asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of CYSKP which are preferably at least 5 to about 15 amino acids in

length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of CYSKP. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with
5 the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which, when bound to CYSKP, decreases the
10 amount or the duration of the effect of the biological or immunological activity of CYSKP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of CYSKP.

The term "antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that
15 bind CYSKP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and
20 keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on
25 the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the
30 complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the

capability of the natural, recombinant, or synthetic CYSKP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" and "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the
5 complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which
10 depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution.
15 Compositions comprising polynucleotide sequences encoding CYSKP or fragments of CYSKP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

20 "Consensus sequence" refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using the XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI). Some sequences have been both extended and
25 assembled to produce the consensus sequence.

The term "correlates with expression of a polynucleotide" indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding CYSKP, by northern analysis is indicative of the presence of nucleic acids encoding CYSKP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding CYSKP.

30 A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide

encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

5 The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization
10 assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to
15 one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

20 The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Madison WI) which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) *Gene* 73:237-244.) Parameters
25 for each method may be the default parameters provided by MEGALIGN or may be specified by the user. The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in
30 sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) *Methods Enzymol.* 183:626-645.) Identity between sequences can also be determined

by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

5 The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

10 The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate
15 to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

"Immune response" can refer to conditions associated with inflammation, trauma, immune
20 disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" and "array element" in a microarray context, refer to hybridizable
25 polynucleotides arranged on the surface of a substrate.

The term "modulate" refers to a change in the activity of CYSKP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of CYSKP.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide,
30 oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:17-32, for example, as

distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:17-32 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:17-32 from related polynucleotide sequences. A fragment of SEQ ID NO:17-32 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:17-32 and the region of SEQ ID NO:17-32 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

The terms "operably associated" and "operably linked" refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding CYSKP, or fragments thereof, or CYSKP itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the

antibody.

The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other
5 conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free,
10 preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters,
15 chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various
20 methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of
25 replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of CYSKP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine).
30 More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to CYSKP. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species.

10 Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

THE INVENTION

The invention is based on the discovery of new human cytoskeleton associated proteins (CYSKP), the polynucleotides encoding CYSKP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding CYSKP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each CYSKP were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. The clones in column 5 were used to assemble the consensus nucleotide sequence of each CYSKP and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows homologous sequences as identified by BLAST analysis; and column 7 shows analytical methods used to characterize each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding CYSKP. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists fragments of the nucleotide sequences of column 1. These

fragments are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:17-32 and to distinguish between SEQ ID NO:17-32 and related polynucleotide sequences. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides. Column 3 lists tissue categories which express CYSKP as a fraction of total tissues expressing CYSKP.

- 5 Column 4 lists diseases, disorders, or conditions associated with those tissues expressing CYSKP as a fraction of total tissues expressing CYSKP. Column 5 lists the vectors used to subclone each cDNA library.

Of particular note is the expression of SEQ ID NO:31 in nervous tissues and the expression of SEQ ID NO:32 in musculoskeletal tissues.

- 10 The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding CYSKP were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

- The invention also encompasses CYSKP variants. A preferred CYSKP variant is one which
15 has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the CYSKP amino acid sequence, and which contains at least one functional or structural characteristic of CYSKP.

- The invention also encompasses polynucleotides which encode CYSKP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected
20 from the group consisting of SEQ ID NO:17-32, which encodes CYSKP.

- The invention also encompasses a variant of a polynucleotide sequence encoding CYSKP. In particular, such a variant polynucleotide sequence will have at least about 70%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding CYSKP. A particular aspect of the invention encompasses a
25 variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:17-32 which has at least about 70%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:17-32. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural
30 characteristic of CYSKP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding CYSKP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide

sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring CYSKP, and all such variations are to be considered as being specifically disclosed.

5 Although nucleotide sequences which encode CYSKP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring CYSKP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding CYSKP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the
10 peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CYSKP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

15 The invention also encompasses production of DNA sequences which encode CYSKP and CYSKP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding CYSKP or any fragment thereof.

20 Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:17-32 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM
25 NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily
30 include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment,

hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Perkin-Elmer). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Perkin-Elmer), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding CYSKP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences,

such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown
5 sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction
10 enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3066.) Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries
15 and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

20 When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

25 Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate
30 software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof

which encode CYSKP may be cloned in recombinant DNA molecules that direct expression of CYSKP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express CYSKP.

5 The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter CYSKP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-
10 mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding CYSKP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 7:215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 7:225-232.)
15 Alternatively, CYSKP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of CYSKP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other
20 proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH
25 Freeman, New York NY.)

In order to express a biologically active CYSKP, the nucleotide sequences encoding CYSKP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers,
30 constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding CYSKP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CYSKP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding CYSKP and its initiation codon and

upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding CYSKP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding CYSKP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding CYSKP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding CYSKP can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding CYSKP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of CYSKP are needed, e.g. for the production of antibodies, vectors which direct high level expression of CYSKP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of CYSKP. A number of vectors

containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 5 1995, supra; Grant et al. (1987) *Methods Enzymol.* 153:516-54; and Scorer, C. A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of CYSKP. Transcription of sequences encoding CYSKP may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 10 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology 15 (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding CYSKP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain 20 infective virus which expresses CYSKP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of 25 DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression 30 of CYSKP in cell lines is preferred. For example, sequences encoding CYSKP can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to

confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These
5 include, but are not limited to, the herpes simplex virus thymidine kinase and adenine
phosphoribosyltransferase genes, for use in *tk* or *apv* cells, respectively. (See, e.g., Wigler, M. et al.
(1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or
herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to
methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* or *pat*
10 confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g.,
Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-3570; Colbere-Garapin, F. et al. (1981) J.
Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which
alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc.
Natl. Acad. Sci. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins
15 (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate
luciferin may be used. These markers can be used not only to identify transformants, but also to
quantify the amount of transient or stable protein expression attributable to a specific vector system.
(See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is
20 also present, the presence and expression of the gene may need to be confirmed. For example, if the
sequence encoding CYSKP is inserted within a marker gene sequence, transformed cells containing
sequences encoding CYSKP can be identified by the absence of marker gene function. Alternatively,
a marker gene can be placed in tandem with a sequence encoding CYSKP under the control of a
single promoter. Expression of the marker gene in response to induction or selection usually
25 indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding CYSKP and that
express CYSKP may be identified by a variety of procedures known to those of skill in the art. These
procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR
amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or
30 chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of CYSKP using either
specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques
include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and
fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing

monoclonal antibodies reactive to two non-interfering epitopes on CYSKP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St Paul MN, Sect. IV; Coligan, J. E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and
5 Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding CYSKP
10 include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding CYSKP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety
15 of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding CYSKP may be cultured under
20 conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CYSKP may be designed to contain signal sequences which direct secretion of CYSKP through a prokaryotic or eukaryotic cell membrane.

25 In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different
30 host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid

sequences encoding CYSKP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric CYSKP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of CYSKP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the CYSKP encoding sequence and the heterologous protein sequence, so that CYSKP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled CYSKP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of CYSKP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A peptide synthesizer (Perkin-Elmer). Various fragments of CYSKP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of CYSKP and human cytoskeleton associated proteins. In addition, the expression of CYSKP is closely associated with cancer, cell proliferation, inflammation, immune response, musculoskeletal, nervous, reproductive, cardiovascular, and gastrointestinal tissues. Therefore, CYSKP appears to play a role in cell proliferative, autoimmune/inflammatory, vesicle trafficking,

neurological, cell motility, reproductive, and muscle disorders. In the treatment of disorders associated with increased CYSKP expression or activity, it is desirable to decrease the expression or activity of CYSKP. In the treatment of disorders associated with decreased CYSKP expression or activity, it is desirable to increase the expression or activity of CYSKP.

5 Therefore, in one embodiment, CYSKP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, 10 polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory 15 disorder such as acquired immunodeficiency syndrome (AIDS), actinic keratosis, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, 20 diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, mixed connective tissue disease (MCTD), myelofibrosis, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, 25 polycythemia vera, polymyositis, primary thrombocythemia, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a vesicle trafficking disorder such 30 as cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes mellitus, diabetes insipidus, hyper- and hypoglycemia, Grave's disease, goiter, Cushing's disease, and Addison's disease, gastrointestinal disorders including ulcerative colitis, gastric and duodenal ulcers, other conditions associated with abnormal vesicle trafficking, including acquired immunodeficiency syndrome (AIDS), allergies including hay fever, asthma, and urticaria (hives), autoimmune hemolytic

- anemia, proliferative glomerulonephritis, inflammatory bowel disease, multiple sclerosis, myasthenia gravis, rheumatoid and osteoarthritis, scleroderma, Chediak-Higashi and Sjogren's syndromes, systemic lupus erythematosus, toxic shock syndrome, traumatic tissue damage, and viral, bacterial, fungal, helminthic, and protozoal infections; a neurological disorder such as epilepsy, ischemic
- 5 cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial
- 10 thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy,
- 15 neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy,
- 20 tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a cell motility disorder such as ankylosing spondylitis, Chediak-Higashi syndrome, Duchenne and Becker muscular dystrophy, intrahepatic cholestasis, myocardial hyperplasia, cardiomyopathy, early onset periodontitis, cancers such as adenocarcinoma, ovarian carcinoma, and chronic myelogenous
- 25 leukemia, and bacterial and helminthic infections; and a heart and skeletal muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, and ethanol myopathy.

- 30 In another embodiment, a vector capable of expressing CYSKP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified CYSKP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat

or prevent a disorder associated with decreased expression or activity of CYSKP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of CYSKP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP including, but not limited to, those listed above.

In a further embodiment, an antagonist of CYSKP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CYSKP. Examples of such disorders include, but are not limited to, those cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, and heart and skeletal muscle disorders described above; a reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis, cancer of the breast, fibrocystic breast disease, and galactorrhea, a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; and a smooth muscle disorder. A smooth muscle disorder is defined as any impairment or alteration in the normal action of smooth muscle and may include, but is not limited to, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia. Smooth muscle includes, but is not limited to, that of the blood vessels, gastrointestinal tract, heart, and uterus. In one aspect, an antibody which specifically binds CYSKP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express CYSKP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding CYSKP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CYSKP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic

efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of CYSKP may be produced using methods which are generally known in the art. In particular, purified CYSKP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind CYSKP. Antibodies to CYSKP may
5 also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans,
10 and others may be immunized by injection with CYSKP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in
15 humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to CYSKP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the
20 entire amino acid sequence of a small, naturally occurring molecule. Short stretches of CYSKP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to CYSKP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not
25 limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the
30 splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce CYSKP-specific single

chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) Proc. Natl. Acad. Sci. 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte
5 population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86: 3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for CYSKP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin
10 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
15 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between CYSKP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering CYSKP epitopes is preferred, but a competitive binding assay may
20 also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for CYSKP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of CYSKP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions.
25 The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple CYSKP epitopes, represents the average affinity, or avidity, of the antibodies for CYSKP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular CYSKP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in
30 which the CYSKP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of CYSKP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington, DC; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to

Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of CYSKP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, *supra*, and Coligan et al. *supra*.)

In another embodiment of the invention, the polynucleotides encoding CYSKP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding CYSKP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding CYSKP. Thus, complementary molecules or fragments may be used to modulate CYSKP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding CYSKP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding CYSKP. (See, e.g., Sambrook, *supra*; Ausubel, 1995, *supra*.)

Genes encoding CYSKP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding CYSKP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding CYSKP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful

because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-
5 177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example,
10 engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding CYSKP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides,
15 corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared
20 by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding CYSKP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA
25 constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase
30 linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved
5 using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

10 An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of CYSKP, antibodies to CYSKP, and mimetics, agonists, antagonists, or inhibitors of CYSKP. The compositions may be administered alone or in combination with at least one other agent, such as a
15 stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial,
20 intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on
25 techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees,
30 capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol,

and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, 5 such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to 10 characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, 15 the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances 20 which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable 25 stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner 30 that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acids. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding

free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of CYSKP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example CYSKP or fragments thereof, antibodies of CYSKP, and agonists, antagonists or inhibitors of CYSKP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100.000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind CYSKP may be used for the diagnosis of disorders characterized by expression of CYSKP, or in assays to monitor patients being treated with CYSKP or agonists, antagonists, or inhibitors of CYSKP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for CYSKP include methods which utilize the antibody and a label to detect CYSKP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring CYSKP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of CYSKP expression. Normal or standard values for CYSKP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to CYSKP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of CYSKP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding CYSKP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of CYSKP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of CYSKP, and to monitor regulation of CYSKP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding CYSKP or closely related molecules may be used to identify nucleic acid sequences which encode CYSKP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a

conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding CYSKP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the CYSKP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:17-32 or from genomic sequences including promoters, enhancers, and introns of the CYSKP gene.

Means for producing specific hybridization probes for DNAs encoding CYSKP include the cloning of polynucleotide sequences encoding CYSKP or CYSKP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding CYSKP may be used for the diagnosis of disorders associated with expression of CYSKP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), actinic keratosis, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, mixed connective tissue disease (MCTD), myelofibrosis, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, primary

thrombocythemia, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and

5 trauma; a vesicle trafficking disorder such as cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes mellitus, diabetes insipidus, hyper- and hypoglycemia, Grave's disease, goiter, Cushing's disease, and Addison's disease, gastrointestinal disorders including ulcerative colitis, gastric and duodenal ulcers, other conditions associated with abnormal vesicle trafficking, including acquired immunodeficiency syndrome (AIDS), allergies including hay fever,

10 asthma, and urticaria (hives), autoimmune hemolytic anemia, proliferative glomerulonephritis, inflammatory bowel disease, multiple sclerosis, myasthenia gravis, rheumatoid and osteoarthritis, scleroderma, Chediak-Higashi and Sjogren's syndromes, systemic lupus erythematosus, toxic shock syndrome, traumatic tissue damage, and viral, bacterial, fungal, helminthic, and protozoal infections; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral

15 neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central

20 nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial

25 nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic

30 neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a cell motility disorder such as ankylosing spondylitis, Chediak-Higashi syndrome, Duchenne and Becker muscular dystrophy, intrahepatic cholestasis, myocardial hyperplasia, cardiomyopathy, early onset periodontitis, cancers such as adenocarcinoma, ovarian carcinoma, and chronic myelogenous leukemia, and bacterial and helminthic infections; a heart and

skeletal muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, and ethanol myopathy; a
5 reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea, a disruption of spermatogenesis, abnormal sperm
10 physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; and a smooth muscle disorder. A smooth muscle disorder is defined as any impairment or alteration in the normal action of smooth muscle and may include, but is not limited to, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial
15 infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia. Smooth muscle includes, but is not limited to, that of the blood vessels, gastrointestinal tract, heart, and uterus. The polynucleotide sequences encoding CYSKP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR
20 technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered CYSKP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding CYSKP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide
25 sequences encoding CYSKP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding CYSKP in the
30 sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of CYSKP, a normal or standard profile for expression is established. This may be accomplished by

combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding CYSKP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding CYSKP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced *in vitro*. Oligomers will preferably contain a fragment of a polynucleotide encoding CYSKP, or a fragment of a polynucleotide complementary to the polynucleotide encoding CYSKP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantify the expression of CYSKP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify

genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g.,
5 Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding CYSKP may be
10 used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355; Price,
15 C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene
20 encoding CYSKP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as
25 linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other
30 gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion,

etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, CYSKP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between CYSKP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with CYSKP, or fragments thereof, and washed. Bound CYSKP is then detected by methods well known in the art. Purified CYSKP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding CYSKP specifically compete with a test compound for binding CYSKP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with CYSKP.

In additional embodiments, the nucleotide sequences which encode CYSKP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/131,321, and [Atty Docket No. PF-0594 P, filed September 18, 1998] are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIzol (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8

Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

10 III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Perkin-Elmer) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Perkin-Elmer) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default

parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:17-32. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules

are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding CYSKP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of CYSKP Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:17-32 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar).

Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending
5 the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%)
10 agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-
15 well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was
20 quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulphoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

25 In like manner, the nucleotide sequences of SEQ ID NO:17-32 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:17-32 are employed to screen cDNAs,
30 genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase
35 (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a

SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech).

An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases:

Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

- 5 The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography and compared.

10 VII. Microarrays

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand
15 or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

- 20 Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an
25 appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

30 VIII. Complementary Polynucleotides

- Sequences complementary to the CYSKP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring CYSKP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are
35 designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of CYSKP. To

inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the CYSKP-encoding transcript.

5 IX. Expression of CYSKP

Expression and purification of CYSKP is achieved using bacterial or virus-based expression systems. For expression of CYSKP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express CYSKP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of CYSKP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus 15 (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding CYSKP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (SF9) insect cells in most cases, or human hepatocytes, in some cases. 20 Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, CYSKP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, 25 affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from CYSKP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity 30 purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified CYSKP obtained by these methods can be used directly in the following activity assay.

35 X. Demonstration of CYSKP Activity

A microtubule motility assay for CYSKP activity measures motor domain function. In this assay, recombinant CYSKP is immobilized onto a glass slide or similar substrate. Taxol-stabilized bovine brain microtubules (commercially available) in a solution containing ATP and cytosolic extract are perfused onto the slide. Movement of microtubules as driven by CYSKP motor activity can be visualized and quantified using video-enhanced light microscopy and image analysis techniques. CYSKP activity is directly proportional to the frequency and velocity of microtubule movement.

In the alternative, an assay for CYSKP measures the binding affinity of CYSKP for actin as described by Hammell, R.L. and Hitchcock-DeGregori, S.E. (1997, J. Biol. Chem. 272:22409-22416). CYSKP and actin are prepared from in vitro recombinant cDNA expression systems and the N-terminus of CYSKP is acetylated using methods well known in the art. Binding of N-terminal acetyl-CYSKP to actin is measured by cosedimentation at 25°C in a Beckman model TL-100 centrifuge as described. The bound and free CYSKP are determined by quantitative densitometry of SDS-polyacrylamide gels stained with Coomassie Blue. Apparent binding constants (K_{app}) and Hill coefficients (H) are determined by using methods well known in the art to fit the data to the equation as described by Hammell and Hitchcock-DeGregori (1997, supra). The CYSKP:actin ratio, determined using densitometry, is normalized. Hammell and Hitchcock-DeGregori (1997, supra) have shown that saturation of binding corresponds to a CYSKP:actin molar ratio of 0.14, a stoichiometry of 1 CYSKP:7 actin. The binding of CYSKP to actin is proportional to the CYSKP activity.

In the alternative, CYSKP are assayed by their ability to bind to F-actin using a blot overlay system similar to that described by Luna, E.J. et al. (1997, Soc. Gen. Physiol. Ser. 52:3-18). Proteins in plasma membrane-enriched cell extracts containing CYSKP are separated using SDS polyacrylamide gel electrophoresis (10% acrylamide). The gel-separated proteins are transferred to nitrocellulose using methods well known in the art and the blot is washed and pretreated with non-specific blocking agents. [¹²⁵I]-labeled F-actin is prepared and suspended in overlay buffer, then incubated with the blot for at least 16 hours at 4°C. Unbound label is washed with washing buffer, the blot is air dried and subjected to autoradiography for at least one hour. The autoradiograph band corresponding to the expected molecular mass of CYSKP is identified. The amount of observed [¹²⁵I]-labeled F-actin which binds to CYSKP is proportional to the amount of CYSKP present in the sample.

In the alternative, CYSKP activity is associated with its ability to form protein-protein complexes and is measured by its ability to regulate growth characteristics of NIH3T3 mouse fibroblast cells. A cDNA encoding CYSKP is subcloned into an appropriate eukaryotic expression vector. This vector is transfected into NIH3T3 cells using methods known in the art. Transfected

cells are compared with non-transfected cells for the following quantifiable properties: growth in culture to high density, reduced attachment of cells to the substrate, altered cell morphology, and ability to induce tumors when injected into immunodeficient mice. The activity of CYSKP is proportional to the extent of increased growth or frequency of altered cell morphology in NIH3T3
5 cells transfected with CYSKP.

In the alternative, CYSKP activity is measured as ability to bind to microtubules. Microtubules are purified from adult rat brain by reversible assembly (Vallee, R. B. (1982) *Methods Enzymol.* 134:89-104) or the taxol method (Vallee, R. B. (1982) *J. Cell Biol.* 92:435-442) using PEM buffer (100 mM PIPES, pH 6.6, 1mM EGTA, 1mM MgSO₄). To separate the MAPs from tubulin,
10 the pellets from twice-cycled microtubules are resuspended in PEM buffer and applied to a 0.1 M MgSO₄-saturated phosphocellulose column as described by Sloboda, R. D. and Rosenbaum, J. L. ((1982) *Methods Enzymol.* 85:409-416). The fractions containing protein are applied to a second phosphocellulose column. In a total volume of 100 ml, 20 ml of CYSKP (250 mg/ml) is added to 80 ml of whole microtubules (450 mg/ml) or tubulin (300 mg/ml) and incubated at 37 °C for 10 minutes
15 in the presence of 1 mM GTP and 50 mM taxol. The suspension is centrifuged, the supernatant is removed, and the microtubule pellet is resuspended to the original reaction volume in PEM buffer. To assess the partitioning of CYSKP between the supernatant and pellet fractions, equal amounts of supernatant and resuspended pellet are placed in SDS sample buffer and assayed on a 5-20% gradient SDS polyacrylamide gel stained with Coomassie Brilliant Blue. The amount of CYSKP in the pellet
20 fraction is proportional to the binding of CYSKP to microtubules.

In the alternative, CYSKP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) *Biochem. J.* 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled CYSKP, washed, and any wells with labeled CYSKP complex are assayed. Data obtained using different
25 concentrations of CYSKP are used to calculate values for the number, affinity, and association of CYSKP with the candidate molecules.

XI. Functional Assays

CYSKP function is assessed by expressing the sequences encoding CYSKP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a
30 mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing
35 sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a

means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of CYSKP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding CYSKP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding CYSKP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of CYSKP Specific Antibodies

CYSKP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the CYSKP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by,

for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring CYSKP Using Specific Antibodies

Naturally occurring or recombinant CYSKP is substantially purified by immunoaffinity chromatography using antibodies specific for CYSKP. An immunoaffinity column is constructed by covalently coupling anti-CYSKP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing CYSKP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of CYSKP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/CYSKP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and CYSKP is collected.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	17	1285395	COLNNOT16	015834R1 (HUELPOB01), 866407T1 (BRAITUT03), 1232405F6 (LUNGFET03), 1285395H1 (COLNNOT16), 1478554T1 (CORPNOT02), 2103609R6 (BRAITUT02), 2254859R6 (OVRTUT01), 2692529H1 (LUNGNOT23), 2959263H1 (ADRENOT09), 3076303H2 (BONEUNT01), 3367129H1 (CONNTUT04), 3855643H1 (BRAITUT12), 4061729H1 (BRAINOT21), 4082537F6 (CONFNOT02)
2	18	1320252	BLADNOT04	229546R1 (PANCNOT01), 743845R6 (BRAITUT01), 826714T1 (PROSNOT06), 864534R1 (BRAITUT03), 997163R2 (KIDNTUT01), 1320252F6 and 1320252H1 (BLADNOT04), 1349551F1 (LATRTUT02), 1441011F1 (THYRNOT03), 1500649F6 (SINTBST01), 1525416T1 (UCMCL5T01), 1928370R6 (BRSTNOT02), 1932270H1 (COLNNOT16), 3213480F6 (BLADNOT08), 4540043H1 (THYRTMT01)
3	19	1259001	MENITUT03	1259001H1 (MENITUT03), 1550766H1 (PROSNOT06), 1594658F1 (BRAINOT14), 1594658T1 (BRAINOT14), 1653882F6 (PROSTUT08), 1864111F6 (PROSNOT19), 3399605H1 (UTRSNOT16), 3677286H1 (PLACNOT07), 5045012H1 (PLACFER01), 5188326H1 (LUNGTMT04), SATA00218F1, SATA00850F1
4	20	1627027	COLNPOT01	1361332F6 (LUNGNOT12), 1933148H1 (COLNNOT16), 2378239F6 (ISLTNOT01), 2378239T6 (ISLTNOT01), 3433415H1 (PENCNOT05), 3433415X303F1 (PENCNOT05), 4453336H1 (HEAADIR01)
5	21	1905315	OVARNOT07	1504617F1 (BRAITUT07), 1520641F1 (BLADTUT04), 1905315H1 (OVARNOT07), 3282914F6 (HEAONOT05), 3282914T6 (HEAONOT05)
6	22	1997789	BRSTTUT03	833978T1 (PROSNOT07), 13092335R1 (COLNFET02), 1659579F6 (URETUT01), 1734634T6 (COLNNOT22), 2930134F6 (TLYMNOT04), SAEA00063F1
7	23	2303465	BRSTNOT05	411540R6 (BRSTNOT01), 487448F1 (HNT2AGT01), 487448R1 (HNT2AGT01), 647107H1 (BRSTTUT02), 1426319F1 (SINTBST01), 2155735F6 (BRAINOT09), 2155735T6 (BRAINOT09), 2303465H1 (BRSTNOT05)

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragment
8	24	2363178	LUNGFET05	2363178H1 (LUNGFET05), 2590354F6 (LUNGNOT22), 2590354T6 (LUNGNOT22)
9	25	2363327	ADRENOT07	013068R6 (THP1PLB01), 1295235H1 (PGANNOT03), 1445845X13 (PLACNOT02), 1472260R6 (LUNGTUT03), 1474238T6 (LUNGTUT03), 1643970F6 (HEARFET01), 1794319R6 (PROSTUT05), 1868517F6 (SKINBIT01), 2057830R6 (BEPINOT01), 2058164H1 (BEPINOT01), 2363327F6 (ADRENOT07), 2363327H1 (ADRENOT07), 2363327T6 (ADRENOT07), 2877024F6 (THYRNOT10), 2877024T6 (THYRNOT10), 2930751F6 (TLYMNOT04), 3002267F6 (TLYMNOT06)
10	26	2508327	CONUTUT01	2508327H1 (CONUTUT01), 2508327T6 (CONUTUT01), 3743046H1 (THYMNOT08)
11	27	2524555	BRAITUT21	781951H1 (MYOMNOT01), 2524555H1 (BRAITUT21), 3243902H1 (BRAINOT19), 4296903H1 (SCOMDIT01), SAEA01358F1
12	28	2900717	DRGCNOT01	933857R1 (CERVNOT01), 1632793T6 (COLNNOT19), 1909014F6 (CONNTUT01), 2250618R6 (OVARUT01), 2900717F6 (DRGCNOT01), 2900717H1 (DRGCNOT01), 2967545H1 (SCORNOT04), 3506152H1 (ADRENOT11), 4713710H1 (BRAIHCT01)
13	29	3088904	HEAONOT03	990189H1 (COLNNOT11), 2530228H1 (GBLANOT02), 3088904F6 (HEAONOT03), 3088904H1 (HEAONOT03), 3176845T6 (UTRSTUT04)
14	30	3745193	THYMNOT08	2775454H1 (PANCNOT15), 2811439H1 (OVARNOT10), 3745193F6 (THYMNOT08), 3745193H1 (THYMNOT08), 3745193T6 (THYMNOT08)
15	31	3822123	BONSTUT01	736132R6 (TONSNOT01), 1856649F6 (PROSNOT18), 1877413F6 (LEUKNOT03), 3395569T6 (LUNGNOT28), 3577567H1 (BRONNOT01), 3822123H1 (BONSTUT01), 4247960H1 (BRABDIT01)

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
16	32	4217506	ADRENOT15	590362R1 (UTRSNOT01), 973313R6 (MUSCNOT02), 4216992H1 (ADRENOT15), SEJA03360F1

Table 2

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Homologous Sequences	Analytical Methods
1	1005	S15 T194 S402 S548 S614 T673 S7 S39 S151 S159 T180 T223 T530 S647 S658 S682 T730 S744 S746 S748 T766 S828 S854 T879 S890 T952 S58 S208 T212 S323 T381 S449 S518 S543 S544 S884 T944 Y623	N36	L225 to F263 W272 to D300 I321 to Q367 H379 to L408 F440 to K458 S718 to G721	protein 4.1	BLAST ProfileScan PFAM BLOCKS PRINTS
2	1045	T92 S270 S366 S23 T150 T207 T396 S418 T448 T525 S549 S571 S706 T811 S815 S840 S842 S872 S878 T883 S889 T898 S923 S966 S987 S1038 S36 S41 S336 S340 T343 S370 S408 T538 T551 S657 S658 S770 T789 T826 S839 Y542	N152 N495 N919	L47 to F85 W94 to D123 L144 to D190 I196 to I249 F261 to K279 S770 to G773	protein 4.1	BLAST ProfileScan PFAM BLOCKS PRINTS

Table 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Homologous Sequences	Analytical Methods
3	324	T71 T78 S121 S123 S225 T259 S283 T304 S144 S150 S181 T249 S273 S276 S289	N151 N180	Ankyrin repeat: P6-A41; D42-E74; G76-K85	ARF-directed GTPase activating protein (ankyrin-repeat containing, involved in regulation of cytoskeletal organization) [Mus musculus] g4063614	BLAST PFAM BLOCKS_PFAM
4	385	T6 T30 T375 T19 S61 S161 S176	N59 N132 N328 N341		cardiac muscle tensin [Gallus gallus] g619577	BLAST
5	364	T65 T74 T79 S80 T139 T151 T228 T244 T276 T9 T79 T349 Y116	N318		similar to alpha- actinin [Caenorhabditis elegans] g2315828	BLAST
6	395	S158 S94 S130 S213 S214 S251 S283 S296 S348 T19 S20 T46 S121 T250 S285	N62 N317	WASP homology domain 1: M1-L109	ena-VASP like protein [Mus musculus] g1644453	PFAM BLAST

Table 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Homologous Sequences	Analytical Methods
7	523	T213 S140 T157 S215 T245 S251 S286 S516 T518 S57 T342 S398 S405 S427 S453 S483 T484 T503 Y103 Y197 Y297	N410	ATP/GTP-binding site motif A (P loop): G74-T82	dynein light chain A [Gallus sp.] g510249	MOTIFS BLAST
8	348	S32 S55 T104 T153 T183 S213 T223 T249 S34 S41 T51 T52 S166 S293	N86 N164 N233	Tektin signature: R119-E139	tektin C1 [Strongylocentrotus purpuratus] g1353490	PRINTS BLAST
9	731	S117 S136 S162 T168 S219 S249 S390 T451 S665 S694 S15 T292 S313 T559 S703 Y131 Y407 Y490	N125 N134 N205 N551	CAP-Gly domain proteins: G40-C64		BLOCKS
10	147	T100 S137 S138 S9 Y86 Y116	N91		light chain 3 subunit of microtubule- associated proteins 1A and 1B [Rattus norvegicus] g455109	BLAST

Table 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Homologous Sequences	Analytical Methods
11	57	T13 S15		Thymosin beta-4 family: S15-G55	thymosin beta-4 [Mus musculus] g54794	PFAM MOTIFS ProfileScan BLOCKS BLAST
12	452	T8 S36 S75 T94 S117 S237 S246 S311 T358 S406 T4 S208 S216 T239 S295 Y188	N21 N80 N91 N373	ATP/GTP-binding site motif A (P loop): G204-S211 Signal peptide: M1-G34	non-A non-B hepatitis- associated microtubular aggregates protein (p44) [Pan troglodytes] g218576	MOTIFS SPSCAN BLAST
13	281	T76 T50 S60 S207 S212 T213 T234 T249 S259 T274 S120 S155		Tropomyosins: K6-E38; K45-L281	beta-tropomyosin [Mus musculus] g192157	MOTIFS PFAM ProfileScan BLOCKS BLAST
14	92	S16 S23 T45 T60 T71 T85 T78		Tropomyosin: M1-M92	tropomyosin 5 TM-5 [Rattus sp.] g1703676	PFAM ProfileScan BLOCKS BLAST

Table 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Homologous Sequences	Analytical Methods
15	448	T126 T73 T94 S165 T193 S287 S439 T82 S241 T337 Y172	N380	Tubulin: M1-E433 Signal peptide: M1-A32	alpha-tubulin isotype M-alpha-6 [Mus musculus] g202215	MOTIFS PFAM BLOCKS SPSCAN
16	269	T181 S2 T40 S88 S244 T241 S253	N164	Troponin: K73-W215; H252-K269	troponin T fast muscle isoform [Mus musculus] g2340062	PFAM BLOCKS BLAST

Table 3

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
17	549-587	Nervous (0.265) Reproductive (0.229) Cardiovascular (0.145)	Cancer (0.482) Inflammation (0.253)	pINCY
18	882-918	Reproductive (0.220) Nervous (0.207) Gastrointestinal (0.134)	Cancer (0.549) Trauma (0.110) Inflammation (0.098)	pINCY
19	817-864	Reproductive (0.372) Nervous (0.186) Gastrointestinal (0.116)	Cancer and Cell Proliferation (0.651) Inflammation and Immune Response (0.256)	pINCY
20	489-533	Gastrointestinal (0.385) Cardiovascular (0.154) Reproductive (0.154)	Cancer and Cell Proliferation (0.385) Inflammation and Immune Response (0.308)	pINCY
21	50-106	Reproductive (0.220) Hematopoietic/Immune (0.200) Cardiovascular (0.140)	Cancer and Cell Proliferation (0.500) Inflammation and Immune Response (0.360)	pINCY
22	1070-1228	Hematopoietic/Immune (0.211) Reproductive (0.186) Nervous (0.180)	Cancer and Cell Proliferation (0.590) Inflammation and Immune Response (0.360)	PSPORT1
23	250-336	Reproductive (0.291) Gastrointestinal (0.163) Cardiovascular (0.116) Nervous (0.116)	Cancer and Cell Proliferation (0.663) Inflammation and Immune Response (0.337)	PSPORT1

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
24	164-208	Cardiovascular (0.333) Developmental (0.333) Reproductive (0.333)	Inflammation and Immune Response (0.500) Cancer and Cell Proliferation (0.500)	PSPORT1
25	1028-1072	Hematopoietic/Immune (0.286) Reproductive (0.159) Nervous (0.127)	Cancer and Cell Proliferation (0.540) Inflammation and Immune Response (0.413)	pINCY
26	397-516	Gastrointestinal (0.333) Hematopoietic/Immune (0.333) Musculoskeletal (0.333)	Cancer and Cell Proliferation (0.667)	pINCY
27	434-541	Reproductive (0.236) Nervous (0.156) Gastrointestinal (0.148)	Cancer and Cell Proliferation (0.575) Inflammation and Immune Response (0.353)	pINCY
28	1-177	Reproductive (0.269) Hematopoietic/Immune (0.192) Nervous (0.192)	Cancer and Cell Proliferation (0.654) Inflammation and Immune Response (0.462)	pINCY
29		Reproductive (0.339) Gastrointestinal (0.191) Cardiovascular (0.114)	Cancer and Cell Proliferation (0.631) Inflammation and Immune Response (0.288)	pINCY
30	488-532 551-649	Reproductive (0.199) Gastrointestinal (0.144) Nervous (0.144)	Cancer and Cell Proliferation (0.580) Inflammation and Immune Response (0.326)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
31	163-207	Nervous (0.305) Reproductive (0.158) Gastrointestinal (0.137)	Cancer and Cell Proliferation (0.547) Inflammation and Immune Response (0.295)	pINCY
32	99-143	Musculoskeletal (0.280) Developmental (0.160) Reproductive (0.160)	Cancer and Cell Proliferation (0.680) Inflammation and Immune Response (0.280)	pINCY

Table 4

Polynucleotide SEQ ID NO:	Library	Library Comment
17	COLNNOT16	Library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy. Pathology for the associated tumor tissue indicated invasive grade 2 adenocarcinoma, with invasion through the muscularis. One lymph node contained metastasis with extranodal extension. Family history included benign hypertension, atherosclerotic coronary artery disease, breast cancer, and prostate cancer.
18	BLADNOT04	Library was constructed using RNA isolated from bladder tissue of a 28-year-old Caucasian male, who died from a self-inflicted gunshot wound. The patient had a history of alcohol and tobacco use.
19	MENITUT03	Library was constructed using RNA isolated from brain meningioma tissue removed from a 35-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a benign neoplasm in the right cerebellopontine angle of the brain. Patient history included hypothyroidism. Family history included myocardial infarction and breast cancer.
20	COLNPOT01	Library was constructed using RNA isolated from colon polyp tissue removed from a 40-year-old Caucasian female during a total colectomy. Pathology indicated an inflammatory pseudopolyp; this tissue was associated with a focally invasive grade 2 adenocarcinoma and multiple tubovillous adenomas. Patient history included a benign neoplasm of the bowel.
21	OVARNOT07	Library was constructed using RNA isolated from left ovarian tissue removed from a 28-year-old Caucasian female during a vaginal hysterectomy and removal of the fallopian tubes and ovaries. The tissue was associated with multiple follicular cysts, endometrium in a weakly proliferative phase, and chronic cervicitis of the cervix with squamous metaplasia. Family history included benign hypertension, hyperlipidemia, and atherosclerotic coronary artery disease.

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Library	Library Comment
22	BRSTTUT03	Library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multicentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type I diabetes.
23	BRSTNOT05	Library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.
24	LUNGFET05	Library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation from anencephalus.
25	ADRENOT07	Library was constructed using RNA isolated from adrenal tissue removed from a 61-year-old female during a bilateral adrenalectomy. Patient history included an unspecified disorder of the adrenal glands.
26	CONUTUT01	Library was constructed using RNA isolated from sigmoid mesentery tumor tissue obtained from a 61-year-old female during a total abdominal hysterectomy and bilateral salpingo-oophorectomy with regional lymph node excision. Pathology indicated a metastatic grade 4 malignant mixed müllerian tumor present in the sigmoid mesentery at two sites.

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Library	Library Comment
27	BRAITUT21	Library was constructed using RNA isolated from brain tumor tissue removed from the midline frontal lobe of a 61-year-old Caucasian female during excision of a cerebral meningioma. Pathology indicated subfrontal meningothelial meningioma with no atypia. One ethmoid and mucosal tissue sample indicated meningioma. Family history included cerebrovascular disease, senile dementia, hyperlipidemia, benign hypertension, atherosclerotic coronary artery disease, congestive heart failure, and breast cancer.
28	DRGCNOT01	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
29	HEAONOT03	Library was constructed using RNA isolated from aortic tissue removed from a 27-year-old Caucasian female, who died from an intracranial bleed.
30	THYMNOT08	Library was constructed using RNA isolated from thymus tissue removed from a 4-month-old Caucasian male during a total thymectomy and open heart repair of atrioventricular canal defect using hypothermia. The patient presented with a congenital heart anomaly, congestive heart failure, and Down syndrome. Patient history included abnormal thyroid function study and premature birth. Previous procedures included right and left heart angiography.
31	BONSTUT01	Library was constructed using RNA isolated from sacral bone tumor tissue removed from an 18-year-old Caucasian female during an exploratory laparotomy with soft tissue excision. Pathology indicated giant cell tumor of the sacrum. Patient history included a soft tissue malignant neoplasm. Family history included prostate cancer.

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Library	Library Comment
32	ADRENOT15	Library was constructed using RNA isolated from adrenal tissue removed from a Caucasian female fetus, who died from anencephalus after 16-weeks' gestation.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.0E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Althwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less if applicable
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

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ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) <i>J. Mol. Biol.</i> 215:403-410; Altschul, S.F. et al. (1997) <i>Nucleic Acids Res.</i> 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) <i>Proc. Natl. Acad. Sci.</i> 85:2444-2448; Pearson, W.R. (1990) <i>Methods Enzymol.</i> 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489.	ESTs: fasta E value=1.0E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater: fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, <i>Nucl. Acid Res.</i> , 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) <i>Methods Enzymol.</i> 266:88-105; and Altwood, T.K. et al. (1997) <i>J. Chem. Inf. Comput. Sci.</i> 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less if applicable
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